

# “Junk” DNA as a genetic decoy

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It is well known [1, 2, 3] that in most species a large proportion of the genome does not appear to code genes or proteins, or even regulate coding DNA. This leads to the descriptive expression “junk DNA”. Naturally, it is possible that the hidden information in this DNA has simply escaped us so far; however that such sequences have high redundancy (they may, for example, be long repetitions of the same base) gives weight to their characterization as junk. This raises the question: if junk DNA is indeed useless, what might be its evolutionary advantage?

An obvious answer is that there is *no* evolutionary advantage to junk DNA; however its presence doesn’t cause any harm either. In particular the extra metabolic activity it implies may be negligible, because the percentage of metabolic activity associated with DNA replication is very small. Since only features harmful to survival or reproduction are selected out, a neutral accessory such as junk DNA could still survive.

This is certainly a factor [4], and in some insects it has been shown that the genome size is related to the ability to eliminate DNA. However, for it to be the complete answer to this question one would need to prove that eliminating junk DNA by chance (i.e. by random mutation) carries a suitably low probability in all species. Also it is not always true that the energy cost associated with DNA replication is negligible [5].

A much more interesting possibility is that junk DNA may be a positive evolutionary feature, even though it serves no useful direct purpose. In this short note we suggest that its role is to protect the gene. Most significantly its presence may baffle the actions of mutation agents, such as retro-viruses. In the presence of large amounts of junk, a random genetic agent hits junk most of the time; the meaningful pieces of the genome meanwhile “hide” in the foliage. The higher the percentage of junk the higher the protection it affords to directly useful DNA.

The validity of this argument is far from general. It must certainly be part of the story regarding retroviral insertions, which can indeed be found within junk DNA (along with the low-information sequences mentioned above). According to our hypothesis such insertions are missed hits. However the argument is not so clearcut (and in some cases *has* to break down) with regards to environmental mutagens. Then junk DNA only stands a chance of protecting the gene if junk sequences wool around the low density important sequences. Even

then the argument does not apply, for instance, to ionizing radiation. If a harmful photon or cosmic ray crosses  $n$  junk DNA sections before crossing a “good” one, and if  $p \ll 1$  is the probability of interaction with any one of them, then the probability of a harmful mutation is  $p(1 - p)^n \approx p$ , i.e. the junk did nothing to decrease the cross-section. (The reason why this argument does not apply to retroviruses is that  $p$  is not small once the virus penetrates within striking distance of the DNA). So we are not claiming that junk DNA protects the gene against a general mutation; only that this is a factor in some cases.

With this proviso, the hypothesis that junk DNA protects the gene may be tested by considering that the *percentage* of junk DNA varies widely from specie to specie, with *Drosophila* possessing one of the lowest [6] and the salamander one of the highest. This allows us to predict a number of possible correlations. Let us consider first the effect of retro-viruses. If junk DNA acts as a decoy *only* against unwanted retro-viral insertions, then there should be a close link between the number of different retro-viruses attacking a given specie and its percentage of junk DNA (the fact that some junk DNA are viral insertions will induce a feedback complication to this link). The higher the threat, the higher the protection.

However, other factors interfere with this correlation. Although viral insertions are generally bad news, mutations are also useful, supplying natural selection with variety. But mutation is only beneficial as long as it does not over-run the ability of a species to stabilize its positive features. The ideal mutation rate depends directly on how prolifically a given species reproduces and how short its cycles are. The percentage of junk DNA should reflect this optimized mutation rate.

If a large part of the offspring goes to waste anyway, there is no harm in having a lot of mutation in every generation. This is the case for most insects. If on the contrary a species reproduces very little, and it is crucial to preserve a large proportion of the offspring, then mutation has to be severely suppressed, as the species can only rarely afford a random mutation. This is the case for large mammals. Thus there should be an anti-correlation between the reproductive ability of a species and the percentage of junk DNA it contains (this is consistent with known estimates). More directly, there should be an anti-correlation between the natural mutation rates of a species and its percentage of junk DNA.

There certainly are many other factors, together with the number of retro-viruses and the natural ideal mutation rates, determining the level of protection that should be given to useful DNA in a given species. But the point we wish to make in this note is that, whatever the answer, it is likely that junk DNA is an expression of this delicate balance. That junk DNA percentages are at best rough estimates makes a direct comparison futile at this stage. But as our understanding of genomes improves, it should be possible to test this idea.

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## References

- [1] A. E. Mirsky and H. Ris, *J. Gen. Physiol.* **34**, 451 (1951)
- [2] C. Thomas, *Annu. Rev. Genet.* **5**, 237 (1971).
- [3] T. Cavalier-Smith, *The evolution of genome size*. (Wiley, NY).
- [4] Petrov, Dmitri A., Sangster, Todd A., Johnston, J. Spencer, Hartl, Daniel L., Shaw, Kerry L. *Science* **287**, 1060 (2000).
- [5] Castillo-Davis et al, *Nat. Genet.* **31**, 415 (2002).
- [6] B. Charlesworth, *Nature* **358**, 315 (1996).